

## Editor's Introduction to This Issue

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In the post-genome era, understanding protein biomarkers is becoming more important. Indeed, advances in mass spectrometry-based proteomics technologies have enabled the generation of global proteome data from tissue or body fluid samples collected from a broad spectrum of human diseases. In this issue, there are two inspiring review articles on discovering protein biomarkers. Dr. Daehee Hwang's group (DGIST, Korea) comprehensively reviews network-based protein biomarker mining platforms. In this review, they summarize analytical platforms for network-based protein biomarker discovery and key components in the platforms. Dr. Ji Eun Lee (KIST, Korea) introduces neuropeptidomics. Neuropeptides produced from prohormones by selective action of endopeptidases are vital signaling molecules, playing a critical role in a variety of physiological processes, such as addiction, depression, pain, and circadian rhythms. In this paper, they provide an overview of neuropeptides and mass spectrometry-based neuropeptidomic strategies for the identification and quantitation of neuropeptides. Regarding neurobiology, Dr. In Young Choi's group (The Catholic University of Korea) reviews protocols for web

authorization. Developing a database is important to understand the mechanism of neurobiological disorders, including behavioral addiction. In particular, genetic databases require a high level of security and should be designed based on medical information standards. In this respect, they propose the OAuth standard protocol for database access authorization. Dr. Sangsoo Kim's group (Soongsil University, Korea) has developed a detection method for multicopy single-stranded DNA (msDNA), which is extrachromosomal DNA found in many bacterial species. They applied it in scanning NCBI RefSeq bacterial genome sequences. Their work can be a useful tool in studying the distribution, evolution, and physiological role of msDNA. Dr. Seon-Young Kim's group (KRIBB, Korea) suggests that public datasets should not be expected to be error-free and, whenever possible, that we should check the consistency of the data.

For further details, please visit the G&I homepage ([http://www.kogo.or.kr/webapp/kogo\\_publish/genomics\\_and\\_informatics/](http://www.kogo.or.kr/webapp/kogo_publish/genomics_and_informatics/)).

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